

In the specification:

Insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

Replace the paragraph beginning at page 5, line 25 with the following rewritten paragraph:

A CBF1 gene was isolated by reverse transcriptase polymerase chain reaction (RT-PCR) from 3-week-old Arabidopsis leaves as described previously (Chan and Yu (1998) Plant J. 15:685-695). Two primers covering the whole CBF1 coding region were chosen to amplify a 640 bp DNA fragment. The 5' primer (5'-ACGCGTCGACATGAACTCATTTCAGCTTTT3' (SEQ ID NO:1)) and the 3' primer (5'-CGAGCTCTTAGTAACTCCAAAGCGACA3' (SEQ ID NO:2)) were located at the translation initiation site (ATG) and the stop site (TAA) of the CBF1 coding region, respectively. A pfu DNA polymerase (Promega) was used to amplify the DNA fragment to minimize the chance of sequence mutation. The 640 bp PCR product was cloned into the T7Blue(R) vector (Novagen) to form pT7Blue-CBF1 and the DNA sequence was determined by an ABI PRISM 373 automatic DNA sequencing system. The CBF1 cDNA was then cloned into pJD301 (Luehrsen et al. (1992) Methods in Enzymology 216:397-441) by removing its luciferase gene to form the intermediate vector. The fragment containing a CaMV35S promoter, tobacco mosaic virus (TMV) Ω leader, a CBF1 gene and a nos poly(A) was excised by digesting with BamHI and BglII from the intermediate vector and cloned into the BamHI site of pCAMBIA 2301 (Center for the Application of Molecular Biology of International Agriculture, Australia) to form pJLM1. The pCAMBIA 2301 vector contains two other selectable markers, GUS and NPTII genes driven by two separate 35S promoters. Plasmid was transformed into A. tumefaciens strain LBA4404 cells by electroporation.

Replace the paragraph beginning at page 6, line 18 with the following rewritten paragraph:

To identify positive transgenic lines for Southern analysis, genomic DNA from rooted putative transformants growing on MS medium with 100 mg/l kanamycin sulfate was extracted as described previously (Chan et al. (1993) Plant Mol. Biol. 22:491-506). Total RNA isolation,

as well as DNA and Northern blot analyses, was performed as described (Chan et al. (1994) J. Biol. Chem. 269:17635-17641). The β -glucuronidase (GUS) DNA isolated from the BamHI-SacI restriction fragment of plasmid pBI221 (Clontech), and the CBF1 gene isolated from pT7Blue-CBF1 were used as probes. Tomato β -TUBULIN cDNA fragment was isolated by RT-PCR from 3-month-old tomato plant leaves. The 5' primer (5'-CCCGGGCCACACTTGATCCCATTCGT-3' (SEQ ID NO:3), SmaI site underlined) and the 3' primer (5'-CCCGGGCATTCTGTCTGGGTACTCT-3' (SEQ ID NO:4), SmaI site underlined) were chosen to amplify the 539 bp β -TUBULIN partial cDNA fragment. The PCR fragments were cloned into pT7Blue(R) and the DNA sequences were determined by an ABI PRISM 373 automatic DNA sequencing system. CAT1 (GenBank accession number: M93719) was isolated from subtractive hybridization and excised from pT7Blue(R) vector as probes. These fragments were labeled with [α -³²P]dCTP using the random primer method (Feinberg and Vogelstein (1983) Anal. Biochem. 132:6-13). The GUS histochemical staining assay was performed according to previously described methods (Chan et al. (1993) Plant Mol. Biol. 22:491-506). Tomato seeds produced from transgenic tomato plants were collected and selection procedures performed as described above.